Epps, J.

1635 RUSH

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/155,676A

DATE: 04/22/2000
TIME: 01:05:44

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> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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```
 1                                      SEQUENCE LISTING
 2
 3     (1)     General Information:
 4
 5           (i) APPLICANT: WALLACH, David
 6                          MALININ, Nikolai
 7                          BOLDIN, Mark
 8                          KOVALENKO, Andrei
 9                          METT, Igor
10
11          (ii) TITLE OF INVENTION: MODULATORS OF TNF RECEPTOR ASSOCIATED
12                  FACTOR (TRAF), THEIR PREPARATION AND USE
13
14      (iii) NUMBER OF SEQUENCES: 20
15
16       (iv) CORRESPONDENCE ADDRESS:
17            (A) ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.
18            (B) STREET: 624 Ninth Street, N.W., Suite 300
19            (C) CITY: Washington
20            (D) STATE: D.C.
21            (E) COUNTRY: USA
22            (F) ZIP: 20001
23
24        (v) COMPUTER READABLE FORM:
25            (A) MEDIUM TYPE: Floppy disk
26            (B) COMPUTER: IBM PC compatible
27            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29
30       (vi) CURRENT APPLICATION DATA:
31            (A) APPLICATION NUMBER: US 09/155,676
32            (B) FILING DATE: 04-JAN-1999
33            (C) CLASSIFICATION:
34
35      (vii) PRIOR APPLICATION DATA:
36            (A) APPLICATION NUMBER: PCT/IL97/00117
37            (B) FILING DATE: 01-APR-1997
38
39      (vii) PRIOR APPLICATION DATA:
40            (A) APPLICATION NUMBER: IL 117800
41            (B) FILING DATE: 02-APR-1996
42
43      (vii) PRIOR APPLICATION DATA:
44            (A) APPLICATION NUMBER: IL 119133
45            (B) FILING DATE: 26-AUG-1996
46
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47        (viii)  ATTORNEY/AGENT INFORMATION:
48                   (A)  NAME: BROWDY, Roger L.
49                   (B)  REGISTRATION NUMBER: 25,618
50                   (C)  REFERENCE/DOCKET NUMBER: WALLACH=21
51
52          (ix)  TELECOMMUNICATION INFORMATION:
53                   (A)  TELEPHONE: 202-628-5197
54                   (B)  TELEFAX: 202-737-3528
55
56
57   (2)  INFORMATION FOR SEQ ID NO: 1:
58
59          (i)  SEQUENCE CHARACTERISTICS:
60                   (A)  LENGTH: 1906 base pairs
61                   (B)  TYPE: nucleic acid
62                   (C)  STRANDEDNESS: single
63                   (D)  TOPOLOGY: linear
64
65          (ii)  MOLECULE TYPE: cDNA
66
67          (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
68
69   CATTGGGTCA CGCGGTGGCG GCGCTCTAGA ATAGTGGATC CCCCGGGCTG CAGGAATTCG        60
70
71   ATTCGAGGCC ACGAAGGCCG GCGGCGCGGC GCANGCACCG GCCCGGGGAN AGGCNCCATG       120
72
73   AGCGGATCNC NGAACNATGA CAAAAGACAA TTTCTGCTGG AGCGACTGCT GGATGCAGTG       180
74
75   AAACAGTGCC AGATCCGCTT TNGAGGGAGA AAGGAGATTG CCTCGGATTC CGACAGCAGG       240
76
77   GTCACCTGTC TGTGTGCCCA GTTTGAAGCC GTCCTGCAGC ATGGCTTGAA GAGGAGTCGA       300
78
79   GGATTGGCAC TCACAGCGGC AGCGATCAAG CAGGCAGCGG GCTTTGCCAG CAAAACCGAA       360
80
81   ACAGAGCCCG TGTTCTGGTA CTACGTGAAG GAGGTCCTCA ACAAGCACGA GCTGCAGCGC       420
82
83   TTCTACTCCC TGCGCCACAT CGCCTCAGAC GTGGGCCGGG GTCGCGCCTG GCTGCGCTGT       480
84
85   GCCCTCAACG AACACTCCCT GGAGCGCTAC CTGCACATGC TCCTGGCCGA CCGCTGCAGG       540
86
87   CTGAGCACTT TTTATGAAGA CTGGTCTTTT GTGATGGATG AAGAAAGGTC CAGTATGCTT       600
88
89   CCTACCATGG CAGCAGGTCT GAACTCCATA CTCTTTGCGA TTAACATCGA CAACAAGGAT       660
90
91   TTGAACGGGC AGAGTAAGTT TGCTCCCACC GTTTCAGACC TCTTAAAGGA GTCAACGCAG       720
92
93   AACGTGACCT CCTTGCTGAA GGAGTCCACG CAAGGAGTGA GCAGCCTGTT CAGGGAGATC       780
94
95   ACAGCCTCCT CTGCCGTCTC CATCCTCATC AAACCTGAAC AGGAGACCGA CCCTTGCCTG       840
96
97   TCGTGTCCAG GAATGTCAGT GCTGATGCCA AATGCAAAAA GGAGCGGAAG AAGAAAAAGA       900
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99   AAGTGACCAA CATAATCTCA TTTGATGATG AGGAAGATGA GCAGAACTCT GGGGACGTGT       960
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100
101    TTAAAAAGAC ACCTGGGGCA GGGGAGAGCT CAGAGGACAA CTCCGACCGC TCCTCTGTCA         1020
102
103    ATATCATGTC CGCCTTTGAA AGCCCCTTCG GGCCTAACTC CAATGGAATC AGAGCAGCAA         1080
104
105    CTCATGGAAA ATTGATTCCC TGTCTTTGAA CGGGGAGTTT GGGTACCAGA AGCTTGATGT         1140
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107    GAAAAGCATC GATGATGAAG ATGTGGATGA AAACGAAGAT GACGTGTATG GAAACTCATC         1200
108
109    AGGAAGGAAG CACAGGGGCC ACTCGGAGTC GCCCGAGAAG CCACTGGAAG GGAACACCTG         1260
110
111    CCTCTCCCAG ATGCACAGCT GGGCTCCGCT GAAGGTGCTG CACAATGACT CCGACATCCT         1320
112
113    CTTCCCTGTC AGTGGCGTGG GCTCCTACAG CCCAGCAGAT GCCCCCCTCG GAAGCCTGGA         1380
114
115    GAACGGGACA GGACCAGAGG ACCACGTTCT CCCGGATCCT GGACTTCGGT ACAGTGTGGA         1440
116
117    AGCCAGCTCT CCAGGCCACG GAAGTCCTCT GAGCAGCCTG TTACTTCTGC CTCAGTGCCA         1500
118
119    GAGTCCATGA CAATTAGTGA ACTGCGCCAG GCCACTGTGG CCATGATGAA CAGGAAGGAT         1560
120
121    GAGCTGGAGG AGGAGAACAG ATCACTGCGA AACCTGCTCG ACGGTGAGAT GGAGCACTCA         1620
122
123    GCCGCGCTCC GGCAAGAGGT GGACACCTTG AAAAGGAAGG TGGCTGAACA GGAGGAGCGG         1680
124
125    CAGGGCATGA AGGTCCAGGC GCTGGCCAGC TATCTTTGCT ATTTTGTGAG GAGATTCTAA         1740
126
127    CCCCACGTGA GAACCATGTG GTGGAGAAAT GGAGGGAGAG AGAAATCCAA CAGTTCCTGA         1800
128
129    TAGTCTCATT TGAGCTCCTG GATCCAGTCT TTCCTGAAGC TGTGTTTCCT CTGGACTTTT         1860
130
131    CATGTATGTG AGCCAATAAA TTGCTTTCAT TCCTTGAAAA AAAAAA                        1906
132
133    (2)  INFORMATION FOR SEQ ID NO: 2:
134
135         (i)  SEQUENCE CHARACTERISTICS:
136              (A)  LENGTH: 604 amino acids
137              (B)  TYPE: amino acid
138              (C)  STRANDEDNESS: single
139              (D)  TOPOLOGY: linear
140
141    (ii)  MOLECULE TYPE: protein
142
143    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
144
145    Xaa Thr Gly Pro Gly Xaa Gly Xaa Met Ser Gly Ser Xaa Asn Xaa Asp
146    1               5                   10                  15
147
148    Lys Arg Gln Phe Leu Leu Glu Arg Leu Leu Asp Ala Val Lys Gln Cys
149             20                  25                  30
150
151    Gln Ile Arg Phe Xaa Gly Arg Lys Glu Ile Ala Ser Asp Ser Asp Ser
152             35                  40                  45
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153
154    Arg Val Thr Cys Leu Cys Ala Gln Phe Glu Ala Val Leu Gln His Gly
155        50                  55                  60
156
157    Leu Lys Arg Ser Arg Gly Leu Ala Leu Thr Ala Ala Ala Ile Lys Gln
158    65                      70                  75                  80
159
160    Ala Ala Gly Phe Ala Ser Lys Thr Glu Thr Glu Pro Val Phe Trp Tyr
161                    85                  90                  95
162
163    Tyr Val Lys Glu Val Leu Asn Lys His Glu Leu Gln Arg Phe Tyr Ser
164                100                 105                 110
165
166    Leu Arg His Ile Ala Ser Asp Val Gly Arg Gly Arg Ala Trp Leu Arg
167                115                 120                 125
168
169    Cys Ala Leu Asn Glu His Ser Leu Glu Arg Tyr Leu His Met Leu Leu
170        130                 135                 140
171
172    Ala Asp Arg Cys Arg Leu Ser Thr Phe Tyr Glu Asp Trp Ser Phe Val
173    145                 150                 155                 160
174
175    Met Asp Glu Glu Arg Ser Ser Met Leu Pro Thr Met Ala Ala Gly Leu
176                165                 170                 175
177
178    Asn Ser Ile Leu Phe Ala Ile Asn Ile Asp Asn Lys Asp Leu Asn Gly
179                180                 185                 190
180
181    Gln Ser Lys Phe Ala Pro Thr Val Ser Asp Leu Leu Lys Glu Ser Thr
182                195                 200                 205
183
184    Gln Asn Val Thr Ser Leu Leu Lys Glu Ser Thr Gln Gly Val Ser Ser
185        210                 215                 220
186
187    Leu Phe Arg Glu Ile Thr Ala Ser Ser Ala Val Ser Ile Leu Ile Lys
188    225                 230                 235                 240
189
190    Pro Glu Gln Glu Thr Asp Pro Cys Leu Ser Cys Pro Gly Met Ser Val
191                245                 250                 255
192
193    Leu Met Pro Asn Ala Lys Arg Ser Gly Arg Arg Lys Arg Lys Xaa Pro
194                260                 265                 270
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196    Thr Xaa Ser His Leu Met Met Arg Lys Met Ser Arg Thr Leu Gly Thr
197        275                 280                 285
198
199    Cys Leu Lys Arg His Leu Gly Gln Gly Arg Ala Gln Arg Thr Thr Pro
200        290                 295                 300
201
202    Thr Ala Pro Leu Ser Ile Ser Cys Pro Pro Leu Lys Ala Pro Ser Gly
203    305                 310                 315                 320
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RAW SEQUENCE LISTING
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211     Arg Xaa Xaa Arg Cys Gly Xaa Lys Arg Arg Xaa Arg Val Trp Lys Leu
212                 355               360               365
213
214     Ile Arg Lys Glu Ala Gln Gly Pro Leu Gly Val Ala Arg Glu Ala Thr
215         370               375               380
216
217     Gly Arg Glu His Leu Pro Leu Pro Asp Ala Gln Leu Gly Ser Ala Glu
218     385               390               395               400
219
220     Gly Ala Ala Gln Xaa Leu Arg His Pro Leu Pro Cys Gln Trp Arg Gly
221                 405               410               415
222
223     Leu Leu Gln Pro Ser Arg Cys Pro Pro Arg Lys Pro Gly Glu Arg Asp
224                 420               425               430
225
226     Arg Thr Arg Gly Pro Arg Ser Pro Gly Ser Trp Thr Ser Val Gln Cys
227         435               440               445
228
229     Gly Ser Gln Leu Ser Arg Pro Arg Lys Ser Ser Glu Gln Pro Val Thr
230         450               455               460
231
232     Ser Ala Ser Val Pro Glu Ser Met Thr Ile Ser Glu Leu Arg Gln Ala
233     465               470               475               480
234
235     Thr Val Ala Met Met Asn Arg Lys Asp Glu Leu Glu Glu Glu Asn Arg
236                 485               490               495
237
238     Ser Leu Arg Asn Leu Leu Asp Gly Glu Met Glu His Ser Ala Ala Leu
239                 500               505               510
240
241     Arg Gln Glu Val Asp Thr Leu Lys Arg Lys Val Ala Glu Gln Glu Glu
242             515               520               525
243
244     Arg Gln Gly Met Lys Val Gln Ala Leu Ala Ser Tyr Leu Cys Tyr Phe
245         530               535               540
246
247     Val Arg Arg Phe Xaa Pro His Val Arg Thr Met Trp Trp Arg Asn Gly
248     545               550               555               560
249
250     Gly Arg Glu Lys Ser Asn Ser Ser Xaa Xaa Ser His Leu Ser Ser Trp
251                 565               570               575
252
253     Ile Gln Ser Phe Leu Lys Leu Cys Phe Leu Trp Thr Phe His Val Cys
254                 580               585               590
255
256     Glu Pro Ile Asn Cys Phe His Ser Leu Lys Lys Lys
257                 595               600
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/155,676A*

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